

## FIGURE 1

GGCATCTGCCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGG  
CTCTGTTGAGAATC**ATG**CTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTC  
CTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCC  
AGACTGCAGTAAGTGTTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCTGGGC  
CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGT  
CATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGG  
GCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCAT  
TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT  
GAGACCAACATTGGAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGG  
TGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACC  
TTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGAT  
ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGG  
CAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTG  
AAACTAAG**TAA**ATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGAT  
TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAATTATT  
GGTTGCAATGTTGTTACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAA  
GAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATACTCAGCATCTTTATCAC  
TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT  
CACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTTCAGG  
AACCCTGAAGTTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATA  
TGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCG  
TGTTGAGCTTAGCCTTTGACCTTTCCCTTTTGATCCACAAAATACATTAAACTCTGAATTC  
ACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGG  
TTGTAATTTTGTGTATGTTCCCCCACATCGCCCCAACTTCGGATGTGGGGTCAGGAGGTTG  
AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA  
ATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTT  
AGAGAAAGATTTTGACCTGGCTTTAGATAAACTGTGGCAAGAAAAATGTAATGAGCAATAT  
ATGGAAATAAACACACCTTTGTTAAAGATAAAAAAAA

1000 bp scale

## FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686

><subunit 1 of 1, 246 aa, 1 stop

><MW: 26994, pI: 6.43, NX(S/T): 0

MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP  
GIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKEKGYPGIPPELQIAFMASL  
ATHFSNQNSGIIFFSSVETNIGNFFDVM TGRFGAPVSGVYFFTF SMMKHEDVEEVYVYLMHNG  
NTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFS TFAGFLLFETK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **Motif name: Clq domain signature.**

amino acids 137-167

#### **Clq domain proteins.**

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

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[illegible][illegible]

## **FIGURE 4**

MAVKLGTLALLLALGLAQPASARRKLLVFLLDGFRSDYISDEALES LPGFKEIVSRGVKVDY  
LTPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSF DIGVNKDSL MPLWWNGSEPLW  
VTLTKAKRKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA  
IYHERIDVEGHHYGPASPQRKDALKAVD TVLK YMTKWIQERGLQDRLNVIIFSDHGMTDIFW  
MDKVIELNKYISLNDLQQVKDRGPVVS LWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYY  
KKGK FVSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGP  
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALI  
LLFLLA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 100-104, 118-122, 341-345, 404-408

#### **N-myristoylation sites.**

amino acids 148-154, 365-371

#### **Amidation site.**

amino acids 343-347

## **FIGURE 5**

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCC  
CCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGG  
GGGCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCA  
GGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGG  
TGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG  
TGCCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACC  
CTGGAGATAACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT  
GCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG  
CGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCT  
CCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCT  
GCGTGCTGCCCCGTTCAGTGTGAACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGC  
TCCCCAGAGGGCACCCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCCAACACT  
ACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTC  
CAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAA  
AAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTA  
TCACTGGCCTCAGGCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCT  
TAAACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACACATCCCCAAAA

## **FIGURE 6**

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL  
PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDED RYPQKL  
AFAECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGGLPTPGAFAFHTEFIHVP  
VGCTCVLPRSV

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 112-121

**N-myristoylation sites.**

amino acids 32-38, 55-61, 133-139

**Leucine zipper pattern.**

amino acids 3-25

**Homologous region to IL-17.**

amino acids 99-195

[illegible][illegible]

## **FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623

><subunit 1 of 1, 97 aa, 1 stop

><MW: 10160, pI: 6.56, NX(S/T): 0

MLGTTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLP  
LVTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**N-myristoylation sites.**

amino acids 6-11 and 33-38

**Prokaryotic membrane lipoprotein lipid attachment sites.**

amino acids 24-34 and 78-88

103100.1



## FIGURE 9

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTGAGAGGCCGGGGAAGAGAAGCAAAG  
CGCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCT  
AACTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCG  
CGGCACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAG  
CTGGGCTCGGGCGGCGGGAGTAGGGCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTC  
GCGGGCTGCGCCCTGGGCAGAGGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG  
CCGCGATGAGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCC  
TTCTGCGCGCGCGTGGTCAAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTA  
CAAAATGGCCTACTTCCATGAAGTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCTGGCTT  
GTGAGAGTGAGGGAGGAGTCCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAG  
AGCATGTTGCAAAACCTGACAAAACCCGGGACAGGGATTCTGATGGTGATTCTTGATAGG  
GCTTTGGAGGAATGGAGATGGGCAAACATCTGGTGCTGCCAGATCTCTACCAGTGGTCTG  
ATGGAAGCAATTCCCAGTACCGAAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAG  
TGTGTTGTGATGTATCACCACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCA  
GTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTA  
ATCCAACAGCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAAT  
GTGTTTGTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACC  
CCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCTGCATAAAAGTA  
AAGGAAGAACAAAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAA  
GAAAGTGGCATGGAAGTATAAATAACTCATTGACTTGGTTCCAGAATTTTGTAAATCTGGATC  
TGTATAAGGAATGGCATCAGAACAAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGCAA  
GATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAGTAATTTTATATGTCTATTATTTT  
ATTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGTAAAGGATGCAC  
CCAACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTC  
GGGAGTATGTGTGTTAGAAGCAATTCCTTTTATTTCTTTACCTTTTATAAGTTGTTATCTA  
GTCAATGTAATGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAA  
GTGTTTGATAAAAAATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTTCAATACAT  
GCTCTTTTGATTAAAGAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAG  
TACCATAGAAAAAGTTTGTCTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCA  
ATGTCTAGGAAATCTCTTCAGAAATAAGAAGCTATTTTATTAAGTGTGATATAAACCTCCTC  
AAACATTTTACTTAGAGGCAAGGATTGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAA  
TTATTTTGTAGCTTAAATTAACAGATTTTGTAAATATGTAACCTTGTAAATAGGTGCATAA  
ACACTAATGCAGTCAATTTGAACAAAAGAAGTGACATACACAATATAAATCATATGTCTTCA  
CACGTTGCCTATATAATGAGAAGCAGCTCTCTGAGGGTTCTGAAATCAATGTGGTCCCTCTC  
TTGCCCCTAAACAAAGATGGTTGTTGCGGGTTTGGGATTGACACTGGAGGCAGATAGTTGC  
AAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTGACTATATTAGTATACAAAGAGG  
TCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAGACAAGCACAGCACACAGAC  
ATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAATGGGTGGAACCCATCAGTGATCG  
CATATTCATTGATGAGGGTTGCTTGAGATAGAAAATGGTGGCTCCTTTCTGTCTTATCTCC  
TAGTTTCTTCAATGCTTACGCCTTGTCTTCTCAAGAGAAAGTTGTAACCTCTCTGGTCTTCA  
TATGTCCCTGTGCTCCTTTTAACCAAATAAAGAGTTCTTGTCTTCTGGGGGAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30431, pI: 6.79, NX(S/T): 3

MSRVVSLLLGAALLCGHGAFRRVSVSGQKVCFAFDKHPCKMAYFHELSSRVSFQEARLACE  
SEGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDG  
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKKNYICKYEPEINP  
TAPVEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKS  
GRTKTSPNQSTLWISKSTRKESGMEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domain:**

amino acids 214-235

#### **N-glycosylation sites.**

amino acids 86-89 and 255-258

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

#### **N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145  
and 212-217

## FIGURE 11

GGAGAAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG  
CCACAGCCACTGGGCCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTCTGTGCGAGGCCGGCAGGTGG  
GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCCGACC  
GGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC  
AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAAAAACAGCAGATCTTCTCCGTTTCAGAGGACT  
GCCTGGTCTCAACGTCTATAGCCCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTCATGGTATGGGTCCATG  
GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGTGG  
TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT  
TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA  
CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTCC  
ACAGAGCCATCACACAGAGTGGGGTCATCACACCCCAAGGGATCATCGACTCTCACCTTGGCCCCTAGCTCAGA  
AAATCGCAAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAAGAAGGAG  
AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCCTCTCACCGTTGATGGCACTGTCTTCCCCAAAA  
GCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA  
GCTGGCTCATCCCCAGGGGTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT  
CAACACCCGTCTTGACCACTCTGGATGTGCCCCCTGAGATGATGCCACCGTCATAGATGAATACCTAGGAAGCA  
ACTCGGACGCACAAGCCAAATGCCAGGCGTTCAGGAATTCATGGGTGACGTATTCATCAATGTTCCACCGTCA  
GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTCTATGAGTTCAGCATCGACCCAGTTCTTTTG  
CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGTCTTTGTGTTCCGAGGTCCCTTCTCA  
TGGACGAGAGCTCCCGCTGGCCTTTCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATGATGGCCC  
AGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTCACCAGGCGG  
ACAATATCTGGAGATCAACCCAGTGCCACGGGCCGACAGAAGTTCAGGGAGGCCTGGATGCAGTTCTGGTCAG  
AGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAAGGCCAGGAGGACCTCTGAGGCC  
AGGCTGAACCTTCTTGGCTGGGGCAAAACCACTCTTCAAGTGGTGGCAGAGTCCAGCACGGCAGCCCGCCTCTC  
CCCCTGCTGAGACTTTAATCTCCACCAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA  
ATGTCAACAAGGCCGCTCCACCTCTGGGGCATGTACAAGTTCTTCCCTCTCCCTGAAGTGCCTTTCTGCTTT  
CTTCGTGGTAGGTTCTAGCACATTCCTCTAGCTTCTTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTC  
TGGGCTGTGCGGCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT  
CCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCCACTCTGTACCCACACCAGGATCGGGTGGGA  
CCTGGAGCTAGGGGGTGTGTTGCTGAGTGAGTGAGTGAAACACAGAATATGGGAATGGCAGCTGCTGAACCTGAAC  
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGACATTGTCCACCCTGGCCAGAAGGGTGCATGCC  
AATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCGAC  
TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGCTGCCAGTCTGGCCCCCTGCACAAGACAACAGA  
ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCCTCACCAATTCAGCCCCCTGACCCTCAGGACGCTGGATG  
CCAGTCCCAGCCCCAGTGCCGGGTCTCCTCCCTTCTGGCTTGGGGAGACAGTTTCTGGGGAGCTTCCAAG  
AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTCCGGCTATTGTCACA  
GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACCAAGAGTTTTTCAGATGGAAGTGAGAG  
GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGTCTCCTGCGCCTCTGCCTGGGCTCCCACTTTGCA  
GCACTTGAGGAGCCCTTCAACCCGCCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAGGCCGGAGCCAGCT  
CCCTCAGCTTGGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGCGGGCCAG  
AGTGAGTTCCGGGTGGGCGTGGGCTCGGCGGGGCCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCT  
TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTTCTCGCTGGGCTTAGCTGCCTCCCCGCGGGGAGGGCTCGG  
GACCTGCAGCCCTCCATGCCTGACCCTCCCCCACCCTCGTGGGCTCCTGTGCGGCCGGAGCCTCCCCAAGGAG  
CGCCGCCCCCTGCTCCACAGCGCCAGTCCCATCGACCACCAAGGGCTGAGGAGTGCGGGTGCACAGCGCGGGA  
CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG  
GGACTTGAGAAACCTTTATGTCTAGCTAAGGGATTGTAATAACACCGATGGGCACTCTGTATCTAGCTCAAGGTT  
TGTAACACACCAATCAGCACCTGTGTCTAGCTCAGTGTGTTGTGAATGCACCAATCCACACTCTGTATCTGGCT  
ACTCTGGTGGGGAAGTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT  
TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCTGTCAAAACAGACCACTTGACTCTCTGTAAAT  
GGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC  
CCCTCGGGTCCCCCTCCACGCCGTGGAAGCTTTGTTCTTTGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79862

><subunit 1 of 1, 571 aa, 1 stop

><MW: 62282, pI: 5.56, NX(S/T): 1

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVRGRQVGVKGTDRLVNVFLG  
IPFAQPPPLGPDRFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDC  
LVNLVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAYGDVVVVTVQYRLGVLGFF  
STGDEHAPGNQGFLLDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIIISGLVLSPVAAGLF  
HRAITQSGVITTPGIIIDSHWPPLAQKIANLTLACSSSSPAEMVQCLQQKEGEELVLSKKLKNT  
IYPLTVDGTVPFKSPKELLKEKPFHSVPFLMGVNNHEFSWLI PRGWGLLDTMEQMSREDMLA  
ISTPVLTSLDVPPPEMMPTVIDEYLGSNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGS  
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTM  
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW  
HQQKQNRKAQEDL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-27

#### **Transmembrane domain:**

amino acids 226-245

#### **N-glycosylation site.**

amino acids 105-109

#### **N-myristoylation sites.**

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,  
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,  
461-467

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

#### **Carboxylesterases type-B serine active site.**

amino acids 216-232

[illegible][illegible]

## **FIGURE 14**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136

><subunit 1 of 1, 209 aa, 1 stop

><MW: 23909, pI: 9.68, NX(S/T): 0

MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSL  
EKYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFSVLAFPCNQFGESEPRPSKEVES  
FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVVKFWRPEEP  
IEVIRPDIAALVRQVVIKKKEDL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-31

**Glutathione peroxidases signature 2.**

amino acids 104-112

**Glutathione peroxidases.**

amino acids 57-82

10095150-12364

# FIGURE 15

TGTCGCCTGGCCCTCGCCATGCAGACCCCGCGAGCGTCCCCTCCCCGCCCGGCCCTCCTGCTTCTGCTGCTGCTA  
CTGGGGGGGCGCCACGGCCTCTTTCTGAGGAGCCGCCGCCGCTTAGCGTGGCCCCAGGGACTACCTGAACCAC  
TATCCCGTGTGTGTTGGGACGCGGGCCCGACGCCTGACCCCGCAGAAAGGTGCTGACGACCTCAACATCCAGCGA  
GTCCTGCGGGTCAACAGGACGCTGTTTATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAGC  
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTGGATGAAG  
GGCAAACAGGAGGGCGAGTGTGAAACTTCGTAAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC  
GGTTCCAACGCCTTCAACCCGGTGTGCGCAACTACAGCATAGACACCCCTGCAGCCCGTGGAGACAACATCAGC  
GGTATGGCCCGCTGCCCGTACGACCCCAAGCACGCCTAATGTTGCCCTCTTCTCTGACGGGATGCTCTTACAGCT  
ACTGTTACCGACTTCTAGCCATTGATGCTGTCTATCTACCGCAGCCTCGGGGACAGGCCACCCTGCGCACCGTG  
AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC  
TTCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCCGGTGGCCCCGAGTGTGCAAGAAC  
GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGCTCCTTCTGAAGGCGCGGCTCAACTGCTCTGTA  
CCCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGGCGTGGTCAGCCTCGGGGGCGGCCCGTG  
GTCCTGGCCGTTTTTTCCACGCCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG  
GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCCGAGTCCATCTGGACGCCCGGTGCCGAGGATCAG  
GTGCCTCGACCCCGGCCCGGGTGTGCGCAGCCCCCGGGATGCAGTACAATGCCTCCAGCGCCTTGCCGGATGAC  
ATCCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG  
CGACCCCTGATGAGGCACACAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGCCCTTGGGGCAACAGACCGTT  
GTCTTCTGGGTCTGAGGCGGGGACGGTCTCAAGTTCCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT  
GGGCTCAGTGTCTTCTGGAGGAGTTTGAGACCTACCGGCCGACAGGTGTGGACGGCCCCGGCGGTGGCGAGACA  
GGGACGCGGTGCTGAGCTTGGAGCTGGACGCAGCTTCCGGGGGCGCTGCTGGCTGCCCTTCCCCCGCTGCGTGGT  
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAAGACCCCTACTGC  
GGGTGGGCCCCGACGGCTCCTGCATCTTCTCAGCCCCGGGCACAGAGCCGCTTTGAGCAGGACGTGTCCGGG  
GCGAGCACCTCAGGCTTAGGGGACTGCACAGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG  
TCGGTGAACCTGCTGGTAACGTGCTGCGTGGGCGCCCTTCTGGTGGGAGCCGTGGTGTCCGGCTTCAGCGTGGGC  
TGGTTCTGTTGGCCCTCCGTGAGCGGCGGAGCTGGCCCCGGCGCAAGGACAAGGAGGCCATCCTGGCGCACGGGGCG  
GGCGAGGCGGTGCTGAGCGTCAAGCCCTGGGCGAGCGCAGGGCGCAGGGTCCCCGGGGCGGGGCGGAGGCGGT  
GGCGGTGGCGCCGGGGTTCCCCCGAGGCCCTGCTGGCGCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG  
GTGCAGGGCGGGCCCCACGACCTCGGGGCTGCTGCCCCACGCCCGAGCAGACGCCCTGCCGCGAAGCGC  
CTGCCCCACTCCGCACCCGCACCCCCACGCCCTGGGCCCCCGCGCCTGGGACCACGGCCACCCCTGCTCCCGGCC  
TCCGCTTCATCCTCCCTCCTGCTGCTGGCGCCCCCGGGCCCCCGAGCAGCCCCCGCGCCTGGGGAGCCGACC  
CCCCACGGCCGCTCTATGCTGCCCGGCCCGGCCGCGCCTCCACGGCGACTTCCCGCTCACCCCCACGCCAGC  
CCGACCGCCCGGGGGTGGTGTCCGCGCCCCACGGGCCCTTGGACCCAGCCTCAGCCGCCGATGGCCTCCCGCGG  
CCCTGGAGCCCCCCCCGACGGGCAGCCTGAGGAGGCCACTGGGCCCCACGCCCTCCGGCCGCCACCCTGCGC  
CGCACCCACAGTTCAACAGCGCGAGGCCCCGGCCTGGGGACCGCCACCGCGGTGCCACGCCCGGCCGGGCACA  
GACTTGGCCACCTCCTCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTGGCTAGGCCGGGGCCCCCG  
ATGCCTTGGCAGTGCCAGCCACGGGAACAGGAGCGAGAGACGGTGCCAGAACGCCGGGGCCCCGGGGCAACTCCG  
AGTGGGTGCTCAAGTCCCCCCCCGCGACCCACCCGCGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACACCAG  
CTCGCCCTCCCCCTACCCGGGGCCGAGGACGCTGAGACGCTTTGGGGGTGGTGGGCGGGAGGACTTTGCTATG  
GATTTGAGGTTGACCTTATGCGCGTAGGTTTTTGGTTTTTTTTCAGTTTTTGGTTTTCTTTGCGGTTTTCTAAC  
AATTGCACAACCTCCGTTCTCGGGGTGGCGGCAGGCAGGGGAGGCTTGGACGCCGTGGGGAATGGGGGGCCACAG  
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCCAACCCAGGCCCTGGCGTGTGTGGGTGTGCG  
TGCGTGTGCGTGCCGTGTTCTGTGTGCAAGGGGCGGGGAGGTGGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG  
TGGGCGTGTGTGTCAAGTGGGCCACGCGTGCAGGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC  
TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGGTCTCCGAGGTGCCGTTAGGAGTTTGAAC  
CCCCCCTCTGAGAGGGAAGCGGGACAATGCCGGGTTTCAGGCAGGAGACACGAGGAGGGCCTGCCCGGA  
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCTGGGGGGCGGCAAGGTGGGTGGGGCCCCCTCTGTAA  
ATACGGCCCCAGGGTGGTGAAGAGTCCCATGCCACCCGTCCCTTGTGACCTCCCCCTATGACCTCCAGCTGA  
CCATGCATGCCACGTGGCTGGCTGGGTCTCTGCCCTCTTTGGAGTTTGCCTCCCCCAGCCCCCTCCCCATCAAT  
AAAACCTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1036150.43364

## **FIGURE 16**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145

><subunit 1 of 1, 888 aa, 1 stop

><MW: 95285, pI: 8.89, NX(S/T): 8

MQTPRASPPRPALLLLLLLLGGAGHLFPEEPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGA  
DDLNIQVRVLRVNRTLFIGDRDNLRYVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEG  
ECRNFKVLLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALF  
SDGMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFFREI  
AMEFNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCVPGDSHFYFNVLQAVTG  
VVS LGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTVPVPEDQVPR  
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDV  
GAGPWGNQTVVFLGSEAGTVLKFVLRPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGETGQ  
RLLSLELDAASGGLLAAPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGCIFLSPG  
TRAAFEQDVSGASTSGLGDCTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGW  
FVGLRERRELARRKDKEAILAHGAGEAVLSVSRLGERRAQGGPGGGGGGGGAGVPPEALLA  
PLMQNGWAKATLLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLPA  
SASSSLLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRRRVVSAPTG  
PLDPASAADGLPRPWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPG  
TDLAHL LYPGGADRTAPPVP

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domains:**

amino acids 318-339, 598-617

#### **N-glycosylation sites.**

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,  
462-466

#### **Glycosaminoglycan attachment sites.**

amino acids 51-55, 573-577

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

#### **N-myristoylation sites.**

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,  
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,  
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,  
668-674, 669-675, 670-676, 868-874, 879-885



## FIGURE 17

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCTCGGCCGGGACAGC  
AGAACGCCAGGGGACCCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTCG  
CGGAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTG  
CGATCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTC  
ATTTATCGGTGGATCATTTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATT  
GCTTCTTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCCG  
GAGAAGAGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTT  
CTATATTCAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCT  
TCCAGGTGAAAGTCTCAGCACCAGAGGAGCAATTCACTAGAGTTGGAGTCCAGGTTTTAGAC  
CGAAAAGATGGGTCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGT  
GGAAATTAAATTCCAAGGGCAACATGTGGCCAAATCCCATATATTTTAAAGGGCCGGTTT  
ACCATGAGAACTGTGACTGTCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGC  
CCTGAAACCATTGCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAA  
GATTGCAGTAGAAATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAA  
AGGATAACAAGGTTTATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGAT  
GCCATACTACTTTCTTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTT  
GGGAGACTGGCCTTTGGAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCCTGGT  
GTGGCTCCACAGATTCCAAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTG  
GAAACCATGGGCCGGGTAAGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCTCCCTG  
GGAAAGCAAAAATTCCACTGCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGC  
TGGTTAAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTC  
TTTAAACACGATGAAAACCTGTATGGTCCCATTGTGAAACATATTTCAATTTTTTGATTTCTT  
CAAGCATAAGTATCAAATAAATATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGC  
TAGTTGGTGACAGTGTTGTGCTGAAGCAGGATTCATCTACTATGAACATTTTTTACAATGAG  
CTGCAGCCCTGGAAACACTACATTCCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACT  
TAAATGGGCGAAAGATCACGATGAAGAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTG  
CAAGAAATAATCTCATGGGCGATGACATATTCTGTTATTATTTCAAACCTTTTCCAGGAATAT  
GCCAATTTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAAGGGTAGAACCACAGAC  
TGAGGACGACCTCTTCCCTTGTAATGGCATAGGAAAAAGACCAAAGATGAACTCTGATATG  
CAAAATAACTTCTATTAGAATAATGGTGCTCTGAAGACTCTTCTTAACTAAAAAGAAGAATT  
TTTTTAAGTATTAATTCATGGACAATATAAAATCTGTGTGATTGTTTGCAGTATGAAGACA  
CATTTCTACTTATGCAGTATTCTCATGACTGTACTTTAAAGTACATTTTTTAGAATTTTATAA  
TAAAACCACCTTTATTTTAAAGGAAAAAA

## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917

><subunit 1 of 1, 502 aa, 1 stop

><MW: 58043, pI: 7.94, NX(S/T): 2

MFGTLLLYCFFLATVPALAEETGGERQLSPEKSEIWGPGLKADVVLPAFYFYIQAVDTSGNKF  
TSSPGKVFQVKVSAPEEQFTRVGVQVLDRKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKS  
PYILKGPVYHENCDCPLQDSAAWLREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFGQR  
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLDGWPLEKKKSNS  
NIHPIFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR  
DSRKERLELVKLSRKHPOLIDAAFTNFFFFKHDENLYGPIVKHISFFDFFKHKYQINIDGTV  
AAYRLPYLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNLSDLLEKLKWAKDHDEEAKK  
IAKAGQEFARNNLMGDDIFCYFVKLFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRK  
KTKDEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **N-glycosylation sites.**

amino acids 302-306, 414-418

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 243-247, 495-499

#### **Tyrosine kinase phosphorylation site.**

amino acids 341-348

#### **N-myristoylation sites.**

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

#### **Endoplasmic reticulum targeting sequence.**

amino acids 499-504

10036160-13901

## FIGURE 19

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCA  
GCCTAGCGTGTCACG**ATG**CGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCG  
AGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCCCTCTGCC  
AGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGTTCTAACTG  
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG  
ATGATTTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACTTACCTTGTGGAA  
AAAGGAGCATCTCACAGTTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT  
CAAGGCATTGATGACGGGGAGCCTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTC  
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAGCAGCTGGAAAAAGAATAGTCTTT  
TATGGAGATGAAACCTGGGTAAATTAATTCCTCCAAAGCATTTTGTGGAATATGATGGAACAAC  
CTCATTTTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTTGGATAAAG  
TATTA AAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC  
CACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCT  
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTTACCCAATTTGCTGG  
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG  
GTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA  
TCCAAAGCACGTCCAAT**TAG**ACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA  
TTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAG  
CAGTTGAGATTTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC  
GTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAAATGTCAGAAAGATTGCATGGGAACT  
GGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCCTATTCAACCTGGGCTCCAAGGTT  
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA  
GTTCTCACCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGT  
CCCCTGTCATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCG  
TTCACGTCATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTG  
GCGGCAGGCTGCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGG  
CAGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGG  
TGTCCCGACACAGGTGTTACATCTGTGCTGTCAGGTCAGATGCCTCAGTTCTTGGAAGCT  
AGGTTCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTCACAGAGGAACAAGCCC  
CCCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGA  
GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCAC  
TCATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGCGGA  
CGTTTTCTGTTGGAATTCTTAGTCCTTGGCCTCGGACACCTTCATTCGTTAGCTGGGGAGTG  
GTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCAGGATCAAG  
GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCACCCCAACCCTGCACAGCCCTCATC  
CCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTT  
TGTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGC  
CCATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA  
GTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 20**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920

><subunit 1 of 1, 310 aa, 1 stop

><MW: 33875, pI: 7.08, NX(S/T): 2

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTLPP  
PLFSKVVIVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMT  
GSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFFVS  
DYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIGHISGPN SPLIGQKLSEMDSVLMKIHT  
SLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-34

#### **Transmembrane domain:**

amino acids 58-76

#### **N-glycosylation sites.**

amino acids 56-60, 194-198

#### **N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

#### **Amidation site.**

amino acids 154-158

#### **Cell attachment sequence.**

amino acids 205-208

10035012301

## **FIGURE 21**

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATG**GCAAT  
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC  
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATG  
AAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG  
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA  
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACTGAC  
AAATGCAACGCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC  
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA  
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC  
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG  
CACCACCGAGGGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG  
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCT  
CCCCGAGCACTACAGGTCTTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGC  
**ATAG**ACCGCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC  
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL  
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA  
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNEFVPVYIRTCHR  
PSCCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 233-251

#### **N-glycosylation sites.**

amino acids 120-124, 174-178

#### **N-myristoylation sites.**

amino acids 15-21, 84-90

## FIGURE 23

CCCACGCGTCCGGGACAGATGAACTTAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGG  
GAAAGGACAAAAAGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCT  
TTTATGCTGGGAGCTGTGGCTGTAACCAACTAGGAAATAACGTATGCAGCAGCTATGGCTGT  
CAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTTTCTTTTTCTTTTTTGGGGAGTGT  
CCTTGGCAGGTTCTGGGTTTGGACGTTATTTCGGTGACTGAGGAAACAGAGAAAGGATCCTTT  
GTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGAGCTGGCTGCAAGGGGAACCAG  
GGTGGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACACATACCGGGAATTTGCTCA  
CAAATGAGAACTGGACCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTT  
CAAATTTTAATGGATGATCCCTTTCAGATTTACCGGGCTGAGCTGAGAGTCAGGGATATAAA  
TGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAAAATATCAGAAAATACAGCTG  
AAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGGTATCCAA  
AACTACACGATCAGCCCCAACTCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCAT  
GATATATCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCT  
TAACCCTCACAGCGCTGGATGGTGGGCTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATC  
GTTGTCTTGGACGTCAATGACAATGCCCCACAGTTTGCCAGGCTCTGTATGAGACCCAGGC  
TCCAGAAAACAGCCCCATTGGGTTCTTTATTGTTAAGGTATGGGCAGAAGATGTAGACTCTG  
GAGTCAACGCGGAAGTATCCTATTCTTTTTTGTATGCCTCAGAAAATATTTCGAACGACCTTT  
CAAATCAATCCTTTTTCTGGGGAAATCTTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAA  
TTCTTACAAAATAAATATACAGGCAATGGACGGTGGAGGCCCTTTCTGCAAGATGTAGGGTTT  
TAGTGGAAGTATTGGACACCAATGACAATCCCCCTGAACTGATCGTATCATCATTTTCCAAC  
TCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGCTGTTTTTAAGATTAATGACAGAGACTC  
TGGAGAAAATGGAAAGATGGTTTGCTACATTCAAGAGAATCTGCCATTCTACTAAAACCTT  
CTGTGGAGAATTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGAG  
TACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAAAT  
AACGGTCTGGTCTCCGACGTCAATGACAACGCCCGCCTTCACCCAAACCTCCTACACCC  
TGTTTCGTCCGCGAGAACAACAGCCCCCGCCTGCACATCGGCAGCGTCAGCGCCACAGACAGA  
GACTCGGGCACCAACGCCCAGGTACCTACTCGCTGCTGCCGCCCAAGACCCGCACCTGCC  
CCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTGCTGG  
ACTACGAGGCCCTGCAGGCTTTTCGAGTTCCGCGTGGGCGCCACAGACCGCGGCTCCCCCGC  
CTGAGCAGAGAGGCGCTGGTGCCTGCTGGTGGTGGACGCCAACGACAACCTCGCCCTTCGT  
GCTGTACCCGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGC  
CGGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTG  
TCGTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTTCGGTGTGTGGGCGCACAAATGGGGA  
GGTGCACACCGCCAGGCTGCTGAGCGAGCGGACGCGAGCCAAGCACAGGCTCGTGGTGTG  
TCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGAC  
GGCTTCTCCAGCCCTACCTGCCTCTCCCGAGGCGGCCCGGCCAGGCCCAGGCCGAGGC  
CGACTTGCTCACCGTCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTCTCT  
CGGTGCTCCTGTTTCGTGGCGGTGCGGCTGTGCAGGAGGAGCAGGGCGGCCTCGGTGGGTGCG  
TGCTCGGTGCCCCGAGGGTCCTTTTCCAGGGCATCTGGTGGACGTGAGGGGCGCTGAGACCCT  
GTCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCCGGGACCAGTGAGTTCAAGT  
TCTTGAAACCAGTTATTTTCGGATATTTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAAT  
TCCACCTTCCGAAATAGCTTTGGATTAAATATTTCAGTAAAGTCTGTTTTTAGTTTCATATAC  
TTTTGGTGTGTTACATAGCCATGTTTCTATTAGTTTACTTTTTAAATCTCAAATTTAAGTTAT  
TATGCAACTTCAAGCATTATTTTCAAGTAGTATACCCCTGTGGTTTTTACAATGTTTCATCAT  
TTTTTGCATTAATAACAACCTGGGTTTAATTTAATGAGTATTTTTTTTCTAAATGATAGTGTT  
AAGGTTTTAATCTTTCCAACCTGCCAAGGAATTAATTACTATTATATCTCATACAGAAAT  
CTGAGGTTTTGATTCATTTTCAGAGCTTGCACTCTCATGATTCTAATCACTTCTGTCTATAGTG  
TACTTGCTCTATTTAAGAAGGCATATCTACATTTCCAACTCATTCTAACATTCTATATATT  
CGTGTGTTGAAAACCATGTCATTTATTTCTACATCATGTATTTAAAAAGAAATATTTCTCTAC  
TACTATGCTCATGACAAAATGAAACAAAGCATATTGTGAGCAATACTGAACATCAATAATAC  
CCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTTTGGCCAATATTTT  
CTTATGTTAACTTTTGCTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATA  
ATCTGCCTGAAAATGAATAAAAATAAAACATTTTGAATGTGAAAAAAAAAAAAAAAAAAAAA

## FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCFPRQRQVLFLFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAAR  
GTRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVR  
DINDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGNGIQNYTISPNSFFHINISGGD  
EGMIYPELVLDKALDREEQGELSLTLTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYE  
TQAPENSPIGFLIVKVAEDVDSGVNAEVSYSFFDASENIRTTFQINPFSGEIFLRELLDYE  
LVNSYKINIQAAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKIND  
RDSGENGKMVCYIQENLPFLLKPSVENFYILITEGALDREIRAENITITVTDLGTPLRKTE  
HNITVLVSDVNDNAPAFQTQSYTLFVRENNSPALHIGSVSATDRDSTNAQVTYSLLPPQDP  
HLPLASLVSNADNGHLFALRSLDYEAQAFEFVRGATDRGSPALSREALVRVLVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDGFSQPYLPLPEAAPAAQ  
AEADLLTVYLVVALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGHLVDVRGA  
ETLSQSYQYEVCLTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

### Important features of the protein:

#### Signal peptide:

amino acids 1-26

#### Transmembrane domain:

amino acids 687-711

#### N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

#### Glycosaminoglycan attachment site.

amino acids 28-32

#### Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

#### N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,  
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

#### Amidation site.

amino acids 781-785

#### Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

#### Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560



## FIGURE 25

GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCCTC  
GTCTTCCTTCCGGGGGACAACGTGGGTGAGGGCACAGAGAGATATTTAATGTCACCCTCTTG  
GGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTGGGAAAGTTGCTAGAGGCTTC  
AGAACTCCAGCCTA**ATG**GATCCCAAACCTCGGGAGAATGGCTGCGTCCCTGCTGGCTGTGCTG  
CTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCCCTCCCCGCCCCGGCGCTGTTAGAGAA  
AGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGGTGG  
CCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGCTCTTCAGAATGATG  
GCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCCCGTGTGGCCTCGGTGGACATGGGTCC  
TCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGAACCTGGGGA  
GCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTGACCGG  
GGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGGAAACTTTATGGACG  
AGGAGCGACCGACAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCCTTCAGAG  
CCCTGGAGCAAGATCTTCTGTGAATATCAAATTCATCATTGAGGGGATGGAAGAGGCTGGC  
TCTGTTGCCCTGGAGGAACCTTGTGGAAAAAGAAAAGGACCGATTCTTCTCTGGTGTGGACTA  
CATTGTAATTTAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAATCACTTATGGAACCC  
GGGGGAACAGCTACTTCATGGTGGAGGTGAAATGCAGAGACCAGGATTTTCACTCAGGAACC  
TTTGGTGGCATCCTTCATGAACCAATGGCTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGA  
CTCGTCTGGTCATATCCTGGTCCCTGGAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGG  
AAATAAATACATACAAAGCCATCCATCTAGACCTAGAAGAATACCGGAATAGCAGCCGGGTT  
GAGAAATTTCTGTTGATACTAAGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCT  
TTCTATTATGAGGATCGAGGGCGCGTTTGATGAGCCTGGAACCTAAAACAGTCATACCTGGCC  
GAGTTATAGGAAAATTTTCAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAA  
CAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAACAAGATGGTTGT  
TTCCATGACTCTAGGACTACACCCGTGGATTGCAAATATTGATGACACCCAGTATCTCGCAG  
CAAAAAGAGCGATCAGAACAGTGTGTTGGAACAGAACAGATATGATCCGGGATGGATCCACC  
ATTCCAATTGCCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCCGCTGGG  
AGCTGTTGATGATGGAGAACATTCGCAGAATGAGAAAATCAACAGGTGGAACCTACATAGAGG  
GAACCAAATTATTTGCTGCCTTTTTCTTAGAGATGGCCCAGCTCCAT**TAA**TCACAAGAACCT  
TCTAGTCTGATCTGATCCACTGACAGATTACCTCCCCACATCCCTAGACAGGGATGGAAT  
GTAAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAAATGTCTTG  
GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAAATGGTTTAAGGTCC  
CCCACTGCACACCTTCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCCAAGTCCTGT  
GCAATAGCCCCAGGATTGGATTCCTTCCAACCTTTTAGCATATCTCCAACCTTGCAATTTGA  
TTGGCATAATCACTCCGGTTTGGCTTTCTAGGTCCTCAAGTGCTCGTGACACATAATCATTCC  
ATCCAATGATCGCCTTTGCTTTACCACTCTTTCTTTTATCTTATTAATAAAAATGTTGGTC  
TCCACCACTGNCTCCCAA  
AAAAAAAAAA

10036460.42604

```
><subunit 1 of 1, 507 aa, 1 stop
```

MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESD  
SVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDQGSLPIPPVILAEFGSDPTK  
GTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD  
LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY  
FMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY  
KAHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGK  
FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI  
RTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYYIEGTKLF  
AAFFLEMAQLH

Signal peptide:

Transmembrane domain:

N-glycosylation sites.

amino acids 322-326, 382-386, 402-406

## amino acids 400-404

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,  
351-357

## amino acids 140-143

## amino acids 156-167

## FIGURE 27

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCC  
CGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTC**ATG**GGACCTGTGCGGTT  
GGGAATATTGCTTTTCCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGG  
AGGACGATGACACAGAACGCTTGCCCGAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG  
CTACAGGCGGAAGTGAAGTCGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCT  
GGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGG  
CCTTAGAGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCA  
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCCTAGTGCAGAAGGG  
GGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACAT  
ACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTAC  
TTCCACCATCAGGAGCAGCCCCACAAAATTTCTCTGTGAAGGTCATGTGCTCCCAGCTGC  
TGAAACTGCATGTCTACAGGAACTTGGACTGGAAGGAGATCACAGATGGGGAAGAGAAAA  
CAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAG  
ATGACCAAGACAGGAAGCCACCCCAAACCTTGACCGAGAAGATCTT**TGA**ACCCTTGCCCTTTGAG  
CCCCCAGGAGGGGAAGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAG  
CTTTCAGGGTGTGTTTATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACC  
TCAGGCAAGATCCTGGTGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGG  
TCCTGCTCCTAGAGATGAACTCTATCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTA  
CTGAAAGCTTTCCTCTTTAACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGC  
TGTGGGCTTTGGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTTTAGACCCTTCCAAGGAAGA  
GGCCAGAACGGACATTCTCTGCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCA  
GCAAAACCGTGAAGGAGAATGGGACACTGGGTGATGGCCTGGAGTTGCTGATAATTTAGGTGG  
GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGT  
GCTCAACTTTCTATATCGCTATTAACTTTTTTCTTTTTTTCTA

## **FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256

><subunit 1 of 1, 248 aa, 1 stop

><MW: 28310, pI: 4.63, NX(S/T): 0

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAE LSRTGRSREVL  
ELGQVLDTGKRKRHPYPSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMATLK  
GLVQKGVKVDLGIPLELWDEPSVEV TYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEG  
HVLPA AETACLQETWTGKEITDGE EKTEGEEEEQEEEEEEEEEGGDKMTKTGSHPKLDREDL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 106-110

#### **N-myristoylation site.**

amino acids 115-121

#### **Amidation site.**

amino acids 70-74

biochem

## **FIGURE 29**

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT  
CTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTG  
TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA  
GGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGG  
GGAACATTGGCTGCAAGGTTGTTCTGATTGTAACAACACTACAGACAGAAGATCACCTCCTGG  
ATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT  
GGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA  
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAAGGGCCAGGAGTTATCAGCCTAC  
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCA  
GGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAACTCGAGGCTCTTGGAAAATGG  
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAG  
AACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA  
AACCAGGCAGAGATTAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC  
TGCTCACCACCGACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCCTTCTTTTCCAA  
ATTAAAAAAAAAATCATCAA

## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274

><subunit 1 of 1, 223 aa, 1 stop

><MW: 25402, pI: 8.14, NX(S/T): 1

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFPYELGNIGCKVVP  
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLK  
KGKIQQQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSKMDRFLNRFHL  
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 169-173

**Tyrosine kinase phosphorylation site.**

amino acids 59-68

**N-myristoylation sites.**

amino acids 54-60, 83-89, 130-136

**Phosphatidylethanolamine signature.**

amino acids 113-157

1003616012204

## FIGURE 31

GTCGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTCAGTCCCCTGGACTGTAGATAAAGA  
CCCTTTCTTGCCAGGTGCTGAGACAACCACACTATGAGAGGCACTCCAGGAGACGCTGATGG  
TGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG  
CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTG  
TATTGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT  
GTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT  
CCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCC  
ATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAATATAAATGA  
CTGAACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGTCTTAAAGTTTCTGGTTCCTCAATGTGT  
TTTCGTCTACATTTTCTTAGTGTCATTTTACGCTGGTGCTGAGACAGGAGCAAGGCTGCTG  
TTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTCATAGCAACTGAAGAACAGGATG  
TGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTGTCCTCTCAAGCTGGTGCTGTGTAG  
GCCACAAGGCATCTGCATGAGTGACTTTAAGACTCAAAGACCAAACACTGAGCTTTCTTCTA  
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA  
GAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCATCCAGTCTTTAT  
ATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAAGACCTTGTAACA  
AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC  
ATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCA  
TCCAGTCTTTATATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAAG  
ACCTTGTAACAATAAATAATTCTTGTGTTAAGTTAAATCATTTTTGTCCTAATTGTAATGTG  
TAATCTTAAAGTTAAATAAACTTTGTGTATTTATATAATAATAAAGCTAAAACCTGATATAAA  
ATAAAGAAAGAGTAAACTG

## **FIGURE 32**

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQPTL  
QLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY  
NTAFELNIND

### **Signal sequence:**

amino acids 1-17

### **N-myristoylation site.**

amino acids 10-16

### **Cell attachment sequence.**

amino acids 36-39

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## **FIGURE 33**

GCGAGGCTGCACCAGCGCCTGGCACC**ATG**AGGACGCCTGGGCCTCTGCCCCTGCTGCTGCTG  
CTCCTGGCGGGAGCCCCCGCCGCGCGGCCCACTCCCCGACCTGCTACTCCCGCATGCGGGC  
CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGGAGCCAT  
GTGTGAGATACCTGCCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG  
CGGGACTTTGTGGCCTCGCCCCCGTGTTGGAAAGTGGCCCAGGTAGATTCCCTTGAAGGACAA  
AGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTTGGTATTCCTGTTGG  
ATGACTGCAATGCCTTGGAATACCCAATCCCAGTGACTACGGTCCTGCCAGATCGTCAGCGC  
**TAA**GGGAACTGAGACCAGAGAAAGAACCCAAGAGAACTAAAGTTATGTCAGCTACCCAGACT  
TAATGGGCCAGAGCCATGACCCTCACAGGTCTTGTGTTAGTTGTATCTGAAACTGTTATGTA  
TCTCTCTACCTTCTGGAAAACAGGGCTGGTATTCCTACCCAGGAACCTCCTTTGAGCATAGA  
GTTAGCAACCATGCTTCTCATTCCTTGACTCATGTCTTGCCAGGATGGTTAGATACACAGC  
ATGTTGATTTGGTCACTAAAAAGAAGAAAAGGACTAACAAGCTTCACTTTTATGAACAATA  
TTTTGAGAACATGCACAATAGTATGTTTTTATTACTGGTTTAATGGAGTAATGGTACTTTTA  
TTCTTTCTTGATAGAAACCTGCTTACATTTAACCAAGCTTCTATTATGCCTTTTTCTAACAC  
AGACTTTCTTCACTGTCTTTCATTTAAAAAGAAATTAATGCTCTTAAGATATATATTTTACG  
TAGTGCTGACAGGACCCACTCTTTCATTGAAAGGTGATGAAAATCAAATAAAGAATCTCTTC  
ACATGGA

## **FIGURE 34**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011

><subunit 1 of 1, 136 aa, 1 stop

><MW: 15577, pI: 8.88, NX(S/T): 0

MRTPGPLPVLLLLLAGAPAAARPTPPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPRLY  
LDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALEYF  
IPVTTVLPDRQR

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Tyrosine kinase phosphorylation site.**

amino acids 60-69

#### **N-myristoylation site.**

amino acids 16-22

## FIGURE 35

GTCTCCGCGTCACAGGAAGCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGA  
CTTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCA  
GCCGCCAGTCCCGGGCCCCCTCTCCCGCCCCACACCCACCCCTCCTGGCTCTTCCTGTTTTTAC  
TCCTCCTTTTTCATTTCATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCA  
AGCCGAGCGTGGAAGAATGCGGGTTCCTCGGGACCGGCACTTGGATTCTGGTGTAGTGCTCC  
CGATTCAAGCTTTCCCCAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTA  
AGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAAC  
ATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTTTGTGATAACTTGAACCTGC  
TAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCA  
CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGA  
TTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATC  
AACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTAT  
GAAGAAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTAT  
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCT  
CAAAGGAAGCCAACAATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAG  
GCTGGAAAAATACCAGAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGG  
AGAAAACGATGAAACAGTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTA  
AAACCTACAGTGAAGACAACCTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTG  
AAAAGTATTGATTCAGAAAAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAC  
ACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTT  
CCTACCTTGAAAACCTTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAAT  
GCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGA  
CAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAA  
AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTAT  
TTGGAAGCCATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGA  
AGATTATGACCTTTCAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGA  
AAGGCATCCTTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAA  
TGGCAAAAGATCCAGGAGTCTTTCAACTGTTTCAGAAAACATAATATAGCTTAAAACACTTC  
TAATTCTGTGATTAAAAATTTTTTGACCCAAGGGTTATTAGAAAGTGCTGAATTTACAGTAGT  
TAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT  
TGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 36**

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN  
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK  
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQA  
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVT PMAAIQDGLAKGENDET  
VSNTLTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFV  
KMMVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPS EKSHEETDSTKEE  
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLS  
KMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL

### **N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

### **Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

### **N-myristoylation sites:**

amino acids 143-148, 239-244

## FIGURE 37

GTTGCTCCGGCGGCGCTCGGGGAGGGAGCCAGCAGCCTAGGGCCTAGGCCCGGGGCCACC**ATG**  
GCGCTGCCTCCAGGCCAGCCGCCCTCCGGCACACACTGCTGCTCCTGCCAGCCCTTCTGAG  
CTCAGGTTGGGGGAGTTGGAGCCACAAATAGATGGTCAGACCTGGGCTGAGCGGGCACTTC  
GGGAGAATGAACGCCACGCCTTCACCTGCCGGGTGGCAGGGGGCCTGGCACCCCCAGATTG  
GCCTGGTATCTGGATGGACAGCTGCAGGAGGCCAGCACCTCAAGACTGCTGAGCGTGGGAGG  
GGAGGCCTTCTCTGGAGGCACCAGCACCTTCACTGTCACTGCCATCGGGCCCAGCATGAGC  
TCAACTGCTCTCTGCAGGACCCCAGAAGTGGCCGATCAGCCAACGCCTCTGTCATCCTTAAT  
GTGCAATTCAAGCCAGAGATTGCCCAAGTCGGCGCCAAGTACCAGGAAGCTCAGGGCCCAGG  
CCTCCTGGTTGTCCTGTTTGCCCTGGTGCGTGCCAACCCGCCGGCCAATGTCACCTGGATCG  
ACCAGGATGGGCCAGTGACTGTCAACACCTCTGACTTCCTGGTGCTGGATGCGCAGAACTAC  
CCCTGGCTCACCAACCACACGGTGCAGCTGCAGCTCCGCAGCCTGGCACACAACCTCTCGGT  
GGTGGCCACCAATGACGTGGGTGTCAACAGTGCGTCGCTTCAGCCCCAGGCCCTCCCGGC  
ACCCATCTCTGATATCAAGTGACTCCAACAACCTAAAACCTCAACAACGTGCGCCTGCCACGG  
GAGAACATGTCCCTCCCGTCCAACCTTCAGCTCAATGACCTCACTCCAGATTCCAGAGCAGT  
GAAACCAGCAGACCGGCAGATGGCTCAGAACACAGCCGGCCAGAGCTTCTGGACCCGGAGC  
CCGGCGGCCTCCTCACCAGCCAAGGTTTCATCCGCCTCCAGTGCTGGGCTATATCTATCGA  
GTGTCCAGCGTGAGCAGTGATGAGATCTGGCTCT**TGAG**CCCGAGGGCGAGACAGGAGTATTCTC  
TTGGCCTCTGGACACCCTCCCATTCTCCTCAAGGCATCCTCTACCTAGCTAGGTCACCAACGT  
GAAGAAGTTATGCCACTGCCACTTTTGCTTGCCCTCCTGGCTGGGGTGCCCTCCATGTCATG  
CACGTGATGCATTTCACTGGGCTGTAACCCGCAGGGGCACAGGTATCTTTGGCAAGGCTACC  
AGTTGGACGTAAGCCCCTCATGCTGACTCAGGGTGGGCCCTGCATGTGATGACTGGGCCCTT  
CCAGAGGGAGCTCTTTGGCCAGGGGTGTTGAGATGTCATCCAGCATCCAAGTGTTGGCATGGC  
CTGCTGTATACCCACCCACAGTACTCCACAGCACCTTGTACAGTAGGCATGGGGGCGTGCCT  
GTGTGGGGGACAGGGAGGGCCCTGCATGGATTTTCTCCTTCTCTATGTAGCCTTGTT  
CCCTCAGGTAAAATTTAGGACCCTGCTAGCTGTGCAGAACCCAATTGCCCTTTGCACAGAAA  
CCAACCCCTGACCCAGCGGTACCGGCCAAGCACAAACGTCCTTTTGTCTGCACACGTCTCTG  
CCCTTCACTTCTTCTCTTGTCCCCACCTCCTCTTGGGAATTCTAGGTTACACGTTGGACC  
TTCTCTACTACTTCACTGGGCACTAGACTTTTCTATTGGCCTGTGCCATCGCCCAGTATTAG  
CACAAGTTAGGGAGGAAGAGGCAGGCGATGAGTCTAGTAGCACCCAGGACGGCTTGTAGCTA  
TGCATCATTTTCCTACGGCGTTAGCACTTTAAGCACATCCCCTAGGGGAGGGGTGAGTGAG  
GGGCCCAGAGCCCTCTTTGTGGCTTCCCCACGTTTGGCCTTCTGGGATTCACTGTGAGTGTC  
CTGAGCTCTCGGGGTGATGGTTTTTCTCTCAGCATGTCTCCTCCACCACGGGACCCAGCC  
CTGACCAACCCATGGTTGCCTCATCAGCAGGAAGGTGCCCTTCTGGAGGATGGTCGCCACA  
GGCACATAATTCAACAGTGTGGAAGCTTTAGGGGAACATGGAGAAAGAAGGAGACCACATAC  
CCCAAAGTGACCTAAGAACACTTTAAAAAGCAACATGTAAATGATTGGAAATTAATATAGTA  
CAGAATATATTTTTCCCTTGTTGAGATCTTCTTTGTAAATGTTTTTCATGTTACTGCCTAGG  
GCGGTGCTGAGCACACAGCAAGTTTAATAAACTTGACTGAATTCATTTAAAAAAAAAAAAAAAAA  
AAA

## **FIGURE 38**

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPR  
LAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNC SLQDPRSGRSANASVIL  
NVQFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQGPVTVNTSDFLVLDAQN  
YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTSASLPAPGPSRHPSLISSDSNNLKLNNVRLP  
RENMSLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIY  
RVSSVSSDEIWL

### **N-glycosylation sites:**

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,  
251-255, 280-284

### **Glycosaminoglycan attachment site:**

amino acids 23-27

### **Casein kinase II phosphorylation sites:**

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

### **N-myristoylation sites:**

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

## **FIGURE 39**

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCCGGGGCG**ATG**TGGAGCGC  
GGGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGG  
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTC  
AATACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA  
GCAATCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCG  
GCTCGGAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG  
CATGTGCTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCA  
GGAGGTGAGTGCCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCT  
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG  
TTCCTGTCAGTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG  
CATGCCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA  
GTGTGGAGCCCTCTGCAGGTCACGATGAACTC**TGA**GTGTGTGGATGGATGGGTGGATGGAGG  
GTGGCAGGTGGGGCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTC  
AAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA

## **FIGURE 40**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857

><subunit 1 of 1, 221 aa, 1 stop

><MW: 23598, pI: 6.96, NX(S/T): 0

MWSAGRGGAAWPFVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS  
GSGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSP  
SNNQEVSAFGEDGEGDDLDLWTVRCGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQH  
EVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-28

#### **Glycosaminoglycan attachment site.**

amino acids 62-66

#### **N-myristoylation sites.**

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,  
91-97, 190-196

#### **Endoplasmic reticulum targeting sequence.**

amino acids 218-223

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## **FIGURE 41**

GTTGCTATGTTGCCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTTGGAACCACAG  
ACGTGAGCCACTCCACCCAGCCTAAAACCTCATCTTCTTTGGATGAGATGAACACTTTTAAC  
AAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACCTCTAAGGAGGAGCACTGACT  
GAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAAACTTACACA  
GTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGTAGAGCCAGAT  
CGTCATC**ATG**TCTGCATTGTGGCTGCTGCTGGGCCTCCTTGCCCTGATGGACTTGTCTGAAA  
GCAGCAACTGGGGATGCTATGGAAACATCCAAAGCCTGGACACCCCTGGAGCATCTTGTGGG  
ATTGGAAGACGTCACGGCCTGAACTACTGTGGAGTTCGTGCTTCTGAAAGGCTGGCTGAAAT  
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTTGGCCAAAAGTACTGCA  
TGGATCCTGCCGTGATCGCTGGTGTCTTGTCCAGGAAGTCTCCCGGTGACAAAATTCTGGTC  
AACATGGGCGATAGGACTAGCATGGTGCAGGACCCTGGCTCTCAAGCTCCCACATCCTGGAT  
TAGTGAGTCTCAGGTTTCCCAGACAACTGAAGTTCTGACTACTAGAATCAAAGAAATCCAGA  
GGAGGTTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGGG  
GGTGCTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCCTTGC  
ACGAGCCAAGTACCTCAAGAGACATGGCTTC**TAA**CATCTCAGATGAAACCCAAGACCATGAT  
CACATATGCAGCCTCAAATGTTACACAGATAAACTAGCCAAGGGCACCTGTAAGTGGGAAT  
CTGAGTTTGACCTAAAAGTCATTAAAATAACATGAATCCCATTAACCAAAAAAAAAAAAAA

## **FIGURE 42**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867

.><subunit 1 of 1, 194 aa, 1 stop

><MW: 21431, pI: 8.57, NX(S/T): 0

MSALWLLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEIDM  
PYLLKYQPMMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTSWISE  
SQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA  
KYLKRHGF

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **N-myristoylation sites.**

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

#### **Amidation site.**

amino acids 40-44

## **FIGURE 43**

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCCATGAAAG  
CCCTTATGCTGCTCACCCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCAC  
TCCTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGG  
ACAGCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCT  
GTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTG  
ACATATAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCC  
AGCCCTGGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCACTGAG  
ACTCATTCCATTGGCTGCCCCTCCTCCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCT  
CTGTATCCCCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTG  
TTCCGAGTGGTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGT  
CCCTTCCCACCTTCCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCT  
ATACTCTGCTGTCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTG  
TTGTCCCCAGTGAAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA  
AACCAGGCTCCCATATGTACCCCATCCCCCATACTCACCTCTTTCCATTTTGAGTAATAAA  
TGTCTGAGTCTGGAAAAAAAAAAAAAAAAAAAA

4036190-13604

## **FIGURE 44**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878

><subunit 1 of 1, 125 aa, 1 stop

><MW: 13821, pI: 8.60, NX(S/T): 2

MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSN  
LRCGTPEEPCQEAFNQTNRKLGITYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-18

#### **N-glycosylation sites.**

amino acids 77-81, 88-92

#### **N-myristoylation site.**

amino acids 84-90

#### **Ly-6 / u-PAR domain protein signature.**

amino acids 85-98

1003610-1300

## FIGURE 45

ACGGGCCGCGAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGGCTGCAGCTCTGCA  
GTCGGGGCCGTTCCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCT  
ACCGCACCCAGGTTTCGGCCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCCAT  
GGCCGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTC  
TGCTGACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTA  
AAAGCTCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACA  
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTC  
AGAACAAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA  
TACAAATTTGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT  
ACTAAGAGGTTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAAAC  
TGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTCTCTGATTATTATTATAAGTGGTCC  
TCGGCGGATTCCGTAAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT  
TGTAAGTCTATAAGCTGTTCCCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATC  
CTCCATTTTCCCACCGTTACCAGAGATTACCAACTCAGCAGGACCTCCTCCCCCAGGCTTT  
AAGTCTGAGTTCACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGC  
TTTTACAGGACAACAAGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTG  
GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGG  
TACTACCCGTCCTATCCTCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCA  
TGGAGGCTCGGGCAGCTATTCCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAG  
GATATGGTGGTACCAGGAGACGATAAAGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT  
TTTGGATTTTTTCATCACTTTCTCTTTAGAAAAAAAGTACTACCTGTTAACAATTGGGAAAAG  
GGGATATTCAAAGTTCTGTGGTGTATGTCCAGTGTAGCTTTTTTGTATTCTATTATTTGAG  
GCTAAAAGTTGATGTGTGACAAAATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTA  
TATTGCAGTTTTTTGAAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAAC  
CTGTGATGCCCTAAGAAGCATTAAAGAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAA  
AATTTAGTTTTAGGTGGTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA  
TTTGGTATTATATTATTTGATGTTTGCTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAA  
TTATGCTAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTAGTGGTG  
GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTA  
GAAGGTGTTGTGAATGACTCTGTGCTGGCAAAAATGCTTGAAACCTCTATATTTCTTTTCGT  
TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGTTC  
TCTGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAATCA

## **FIGURE 46**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889

><subunit 1 of 1, 339 aa, 1 stop

><MW: 36975, pI: 7.85, NX(S/T): 1

MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIP  
QLKCVGGTAGCDSYTPKVIQCQNKGDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQY  
VLRGSCGLEYNLDYTELGQLKESGKQHGFAFSFYKSSADSCNMSGLITIVVLLGIA  
FVVYKLFSLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGS  
AFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSPYPPGTWNRAYSPL  
HGGSGSYSVCSNSDTKTRTASGYGGTRRR

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 171-190

### **N-glycosylation site.**

amino acids 172-176

### **Glycosaminoglycan attachment sites.**

amino acids 244-248, 259-263, 331-335

### **Tyrosine kinase phosphorylation site.**

amino acids 98-106

### **N-myristoylation sites.**

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,  
270-276, 278-284, 312-318